

1	AGCAGACAGAGGACTCTCATTAAGGAAGG	TGTCCTGTGCCCTGACCCCTACAAGATGCCA	59
		MetPro	2
60	AGAGAAGATGCTCACTTCATCTATGGTTAC	CCCAAGAAGGGGCACGGCCACTCTTACACC	119
3	ArgGluAspAlaHisPheIleTyrGlyTyr	ProLysLysGlyHisGlyHisSerTyrThr	22
120	ACGGCTGAAGAGGCCGCTGGGATCGGCATC	CTGACAGTGATCCTGGGAGTCTTACTGCTC	180
23	<u>ThrAlaGluGluAlaAlaGlyIleGlyIle</u>	<u>LeuThrValIleLeuGlyValLeuLeuLeu</u>	43
181	ATCGGCTGTTGGTATTGTAGAAGACGAAAT	GGATACAGAGCCTTGATGGATAAAAGTCTT	239
44	<u>IleGlyCysTrpTyrCysArgArgAsn</u>	<u>GlyTyrArgAlaLeuMetAspLysSerLeu</u>	62
240	CATGTTGGCACTCAATGTGCCTTAACAAGA	AGATGCCCCACAAGAAGGGTTTGATCATCGG	300
63	HisValGlyThrGlnCysAlaLeuThrArg	ArgCysProGlnGluGlyPheAspHisArg	83
301	GACAGCAAAGTGTCCTCTTCAAGAGAAAAAC	TGTGAACCTGTGGTTCCCAATGCTCCACCT	359
84	AspSerLysValSerLeuGlnGluLysAsn	CysGluProValValProAsnAlaProPro	102
360	GCTTATGAGAAACTCTCTGCAGAACAGTCA	CCACCACCTTATTCACCTTAAGAGCCAGCG	420
103	AlaTyrGluLysLeuSerAlaGluGlnSer	ProProProTyrSerPro	118
421	AGACACCTGAGACATGCTGAAATTATTCT	CTCACACTTTTGCTTGAATTAATACAGAC	479

FIG. 1A

480	ATCTAATGTTCTCCTTTTGGAAATGGTGTAGG	AAAAATGCAAGCCATCTCTAATAATAAGTC	540
541	AGTGTTAAAAATTTTAGTAGGTCGCTAGCA	GTAATAATCATGTGAGGAAATGATGAGAAA	599
600	TATTAATTTGGGAAACTCCATCAATAAAT	GTTGCAATGCATGATACTATCTGTGCCAGA	660
661	GGTAATGTTAGTAAATCCATGGTGTATTT	TCTGAGAGACAGAAATTCAGTGGGTATTCT	719
720	GGGCCATCCAATTTCTCTTTTACTTGAAAT	TTGGCTAATAACAACTAGTCAGGTTTTCG	780
781	AACCTTGACCGACATGAACGTGACACAGAA	TTGTTCCAGTACTATGGAGTGTCACAAAG	839
840	GATACTTTTACAGGTTAAGACAAAGGTTG	ACTGGCCTATTTTATCTGTATCAAGAACAATGT	900
901	CAGCAATGTCCTTTTGTGCTCTAAAAATTCT	ATTATACTACAATAATATATTGTAAAGATC	959
960	CTATAGCTCTTTTTTTTGTGATGGAGTTT	CGCTTTTGTGCCCCAGGCTGGAGTGCAATG	1020
1021	GCGCGATCTTGGCTCACCATAACTCCGCC	TCCCAGGTTCAAGCAATTCTCCTGCCCTTAG	1079
1080	CCTCCTGAGTAGCTGGGATTACAGGCGTGC	GCCACTATGCCCTGACTAAATTTGTAGTTTT	1140
1141	AGTAGAGACGGGTTTCTCCATGTTGGTCA	GGCTGGTCTCAAACCTCCTGACCTCAGGTGA	1199
1200	TCTGCCCCCCTCAGCCTCCCAAAGTCTGG	AATTACAGGCGTGAGCCACCCGCTGGCT	1260
1261	GGATCCTATATCTTAGGTAAGACATATAAC	GCAGTCTAATTACATTTCACTTCAAGGCTC	1319
1320	AATGCTATTCTAACTAATGACAAGTATTTT	CTACTAAACCAGAAATTTGGTAGAAGGATTT	1380
1381	AAATAAGTAAAAGCTACTATGTACTGCCCTT	AGTGCTGATGCCCTGTGTACTGCCCTTAAATG	1439
1440	TACCTATGGCAATTTAGCTCTCTTTGGGTTT	CCAAATCCCTCTCACAAAGAAATGTGCAGAAG	1500
1501	AAATCATAAAGGATCAGAGATTCTGAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1559

FIG. 1B

FIG. 2A

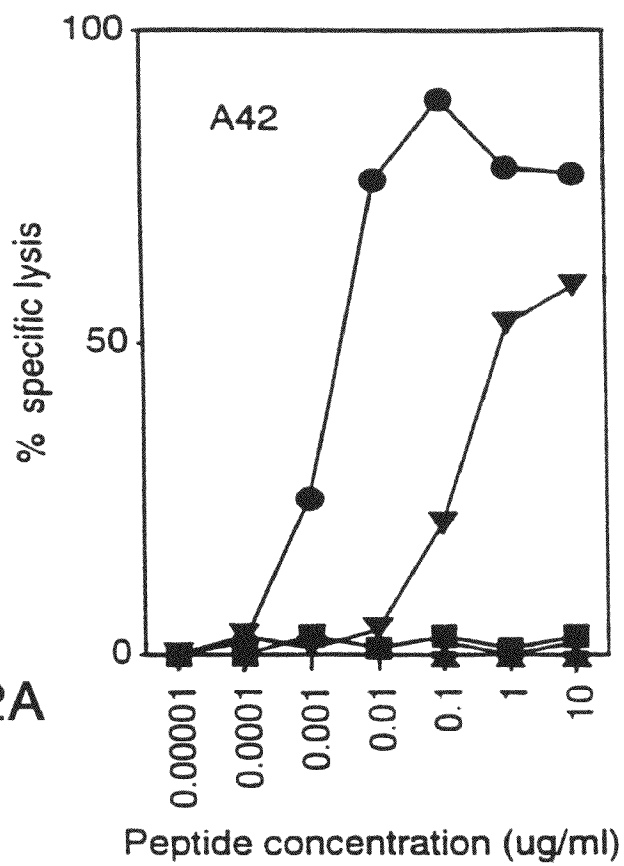
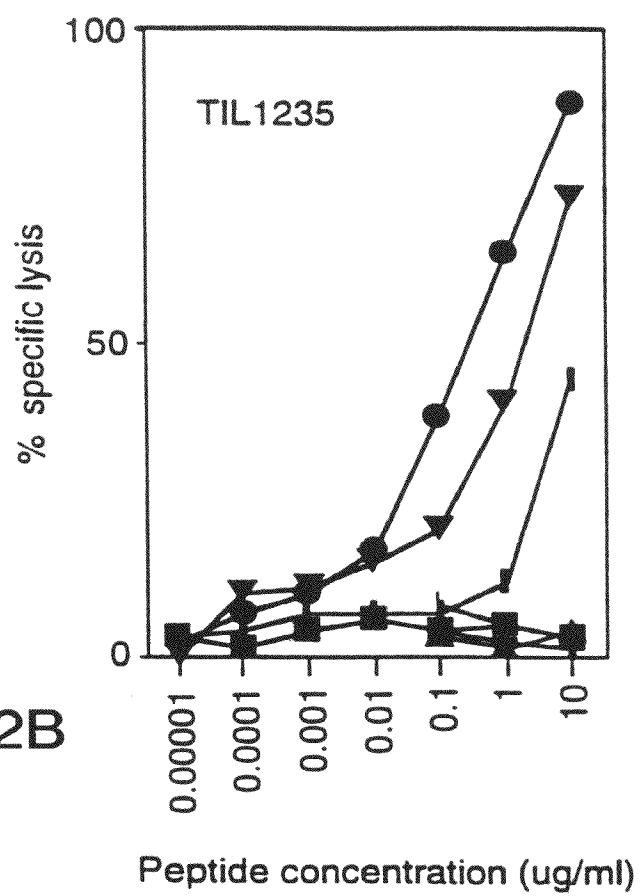
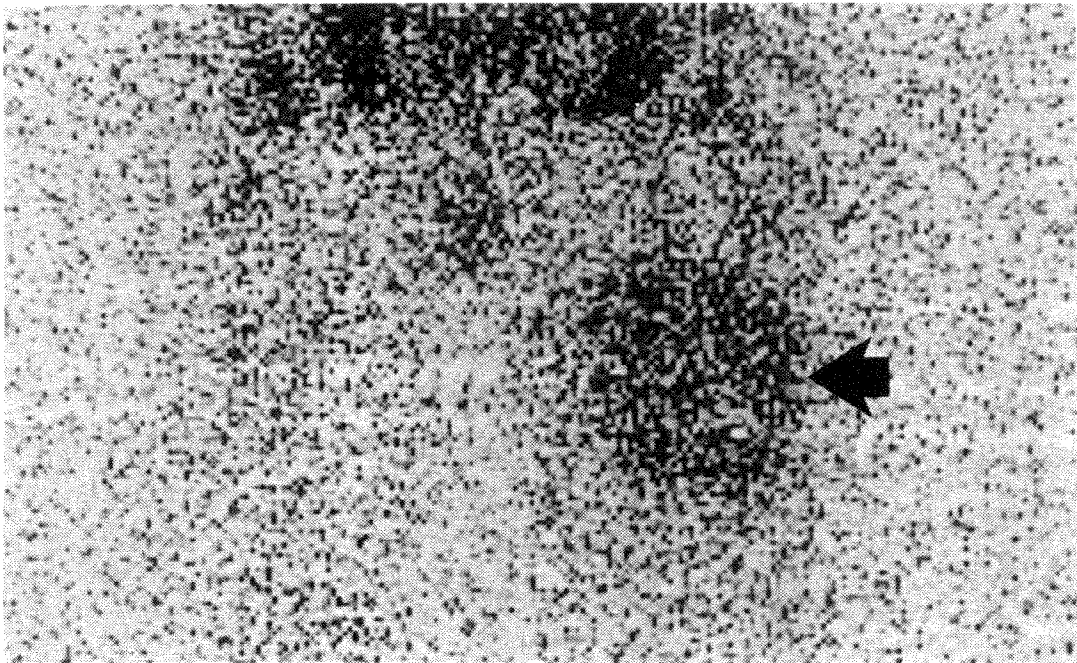


FIG. 2B





**FIG. 3A**

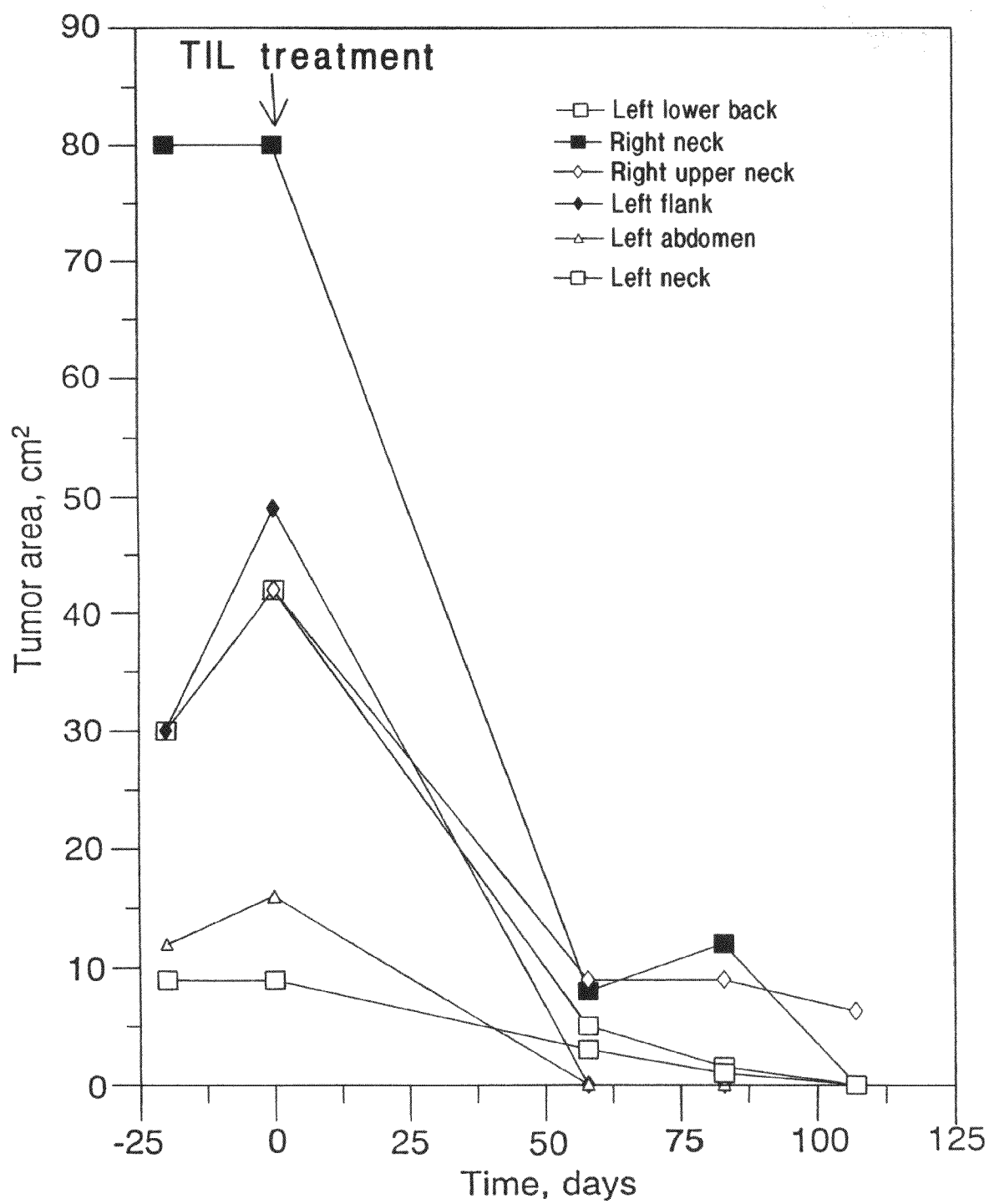


FIG. 3B

GTCGACGGCC	ATTACCAATC	GCGACCGGGA	AGAACA <u>CAAT</u>	40
<u>GGATCTGGTG</u>	CTAAAAAGAT	GCCTTCTTCA	TTTGGCTGTG	80
ATAGGTGCTT	TGCTGGCTGT	GGGGGCTACA	AAAGTACCCA	120
GAAACCAGGA	CTGGCTTGGT	GTCTCAAGGC	AACTCAGAAC	160
CAAAGCCTGG	AACAGGCAGC	TGTATCCAGA	GTGGACAGAA	200
GCCCAGAGAC	TTGACTGCTG	GAGAGGTGGT	CAAGTGTCCC	240
TCAAGGTCAG	TAATGATGGG	CCTACACTGA	TTGGTGCAAA	280
TGCCTCCTTC	TCTATTGCCT	TGAACTTCCC	TGGAAGCCAA	320
AAGGTATTGC	CAGATGGGCA	GGTTATCTGG	GTCAACAATA	360
CCATCATCAA	TGGGAGCCAG	GTGTGGGGAG	GACAGCCAGT	400
GTATCCCCAG	GAAACTGACG	ATGCCTGCAT	CTTCCCTGAT	440
GGTGGACCTT	GCCCATCTGG	CTCTTGGTCT	CAGAAGAGAA	480
GCTTTGTTTA	TGTCTGGAAG	ACCTGGGGCC	AATACTGGCA	520
ATTTCTAGGG	GGCCCAGTGT	CTGGGCTGAG	CATTGGGACA	560
GGCAGGGCAA	TGCTGGGCAC	ACACACCATG	GAAGTGACTG	600
TCTACCATCG	CCGGGGATCC	CGGAGCTATG	TGCCTCTTGC	640
TCATTCCAGC	TCAGCCTTCA	CCATTACTGA	CCAGGTGCCT	680
TTCTCCGTGA	GCGTGTCCCA	GTTGCGGGCC	TTGGATGGAG	720
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACTT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCCTC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAAGTGCAG	AGGCCCTTAA	1000
CACCACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120

FIG. 4A

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAAACCACA	1280
GCTGCACAGG TAACAACCTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIG. 4B

```

1   MDLVLRCLL HLA VIGALLA VGATKVPRNQ DWLGVSRLR TKAWNRLYP
51  EWTEAQLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
101 QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151 YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSPGY
251 LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTTPGQA PTAEPSGTTS
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451 TGSLGPLLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQL CQVLPSPAC
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601 GILLVLMVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651 ENSPLLSGQQ V

```

FIG. 5A

```

Pme117      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20         M-----V-----Q-----L-----.....
gp100        M-----V-----Q-----L-----.....
cDNA25FL     M-----F-----Q-----L-----.....
cDNA25TR          Q-----L-----.....PPQWAAGLSTLI
              1       162       236       274       588       649

```

FIG. 5B

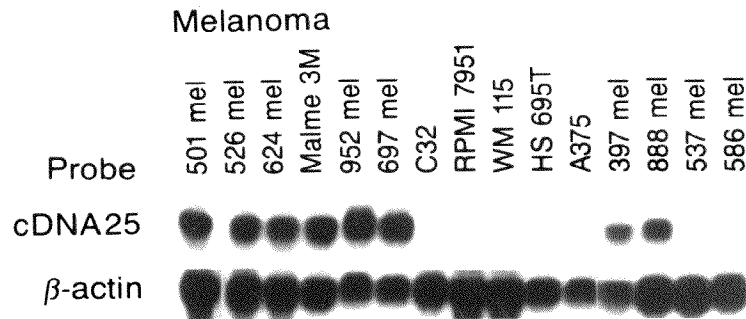


FIG. 6A

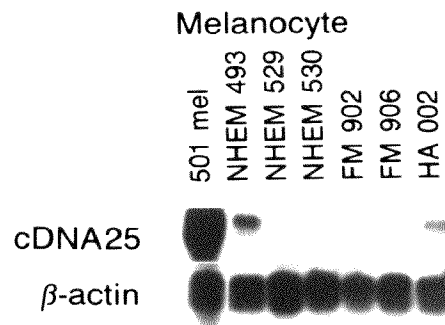


FIG. 6B

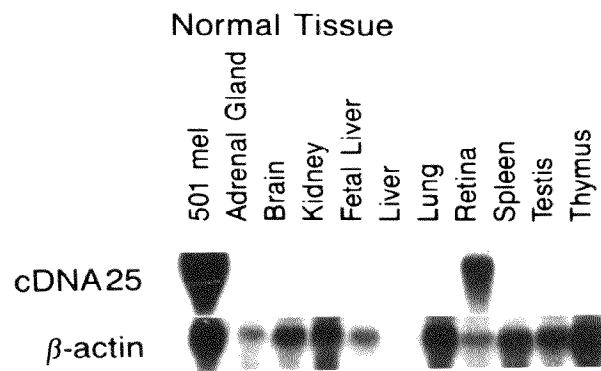


FIG. 6C